

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: An, Gang
O'Hara, S. Mark
Ralph, David
Veltri, Robert
- (ii) TITLE OF INVENTION: BIOMARKERS AND TARGETS FOR DIAGNOSIS,
PROGNOSIS AND MANAGEMENT OF PROSTATE DISEASE
- (iii) NUMBER OF SEQUENCES: 87
- (iv) CORRESPONDENCE ADDRESS:
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(C) CITY: Houston
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(E) COUNTRY: USA
(F) ZIP: 77210
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US Unknown
(B) FILING DATE: Concurrently Herewith
(C) CLASSIFICATION: Unknown
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/692,787
(B) FILING DATE: 31-JUL-1996
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Nakashima, Richard A.
(B) REGISTRATION NUMBER: P-42,023
(C) REFERENCE/DOCKET NUMBER: UROC:018
- (ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 391 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GTCCAGTCGC TCAGAAATTT CCTTTGATGC TTTGAAGTTA TCTCTCTTGG ATCTGCTTCC	60
TCCTTATCGT CTCTACATCC CAAGAACAGA GAGTGAGTCT TCTTTATTTT CTTATCTCTG	120
TTTTTAGCAC AGTATTTGAT ATATAGTGTA GATACTATAA ATGCTTGCTA AACTTTGTCA	180
AATTCCACAT TTTTAAAATA AAAATGAGAA TGAGCTTGTA GTCAACATGG CGTTTGTAAG	240
TTTGGAGTCT ATATATGGTA GATATACATA TTTTAAATC TAAGTGCAAC TTTTCTCTTG	300
ATTATCTTGA AATGCCTTAT CATCTCCACA TTTGCTGTAG GCAGTAGTTT AGTGGGTCCA	360
TTATATCTGC CAACTGATT GTCTTAAATA A	391

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 614 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

CAGTAGTGGC CCCAAATGCC AGGCTGCACT GATATTTATT GGATATAAGA CAAAGGGGCA	60
GGGTAAGGAA TGTGAACCAT CTCCAATAAT AGGTAAGGTC ACATGGGTCA TGTGTCCACT	120
GGACAGGGGG CCCTTCCCTG CCTGGCAGCA GAGGCAGAGA GAGAGAGAAG AGAGAGAGAC	180
AGCTTATGCC ATTATTTCTG CATATCAGAC ATTTAGTACT TTCACTAATT TGCTCCTGCT	240
ATCTAAAAGG CAGAGCCAGG TATACAGGAT GGAACATGAA AGCGGACTAG GAGCGTGACC	300
ACTGAAGCAC AGCATCACAG GGAGACAGGC CTCTGGATAC TGGCCGGGGG GCCCTGACTG	360
ATGTCAAGGC CCTCCACAAG AGTGGAGGAG TTAGTCTTCC TCTAAACTCC CCCGGGGGAA	420
AGGGAGGCTC CTTTTCCAG TCTGCTAAGT AGTGGGTGTT TTTCCCTTGAC ACTGATGCTA	480
CTGCTAGACC ATGGTCCACT TTGCAACAGG CATCTTCCCA GAACTGGTG TTAGTGCTAG	540
ACCAAGCCCT CTGGTGGCCC TGTCCGGGCA TAAGAGAAGG CTCACACTCT TGTCTTCTGG	600
CCACTTCGCA CTAT	614

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 757 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ACAACGACAC ATTCAGGAGT TAAATATTTA TCATCAAACA TTGGATTTTT CCTTAACGCT	60
AGAGATTGCT ACAAATCTTC TGAAGGGTCT CAATGGCTTC AGGCTAAGAA GAGATTTCTC	120
CCTGTTATAA GCAGCAAGAC AAATTAGCCA TTTCACCTCT AACTTCACT AATGATCACA	180
TTCTTTCCAA AAGGAACTCT AGAAGACCAA ATGCCCCGAG TTAAGAACAT CAAAACTAAC	240
CATCTGAAGA AACTTCCCAA GTGTAAGACT CTGCCATTAA AACATTACCG AGAGGGGACT	300
CAAACAGTCT TTTCTTCCCT TTGTCGTGTT TCTTTGCTCC CAGACCCAAG GCACTTGGCG	360
GACAGTACTT GATACAATAA TTTAAAAAGC ACCACTCCCT TCCCACTTTG TAAATACCCA	420
GAAGTCTAAT TGGACCACCC TGAAGCTTAG GACCTACCAG CCATACAAAT AGTAAACTCT	480
GTCCACGATT CACTCATCTG TGTATTTTCT ATAGATGTTT ACTAGGCGTT TGTATATAA	540
AAATACCCCG GCCAGGCACG GTGGCTCACG CCTGTAATCC CAGCACTTTG GGAGGTGGGT	600
GGATCACCTG AGGTCGGGAG TTCGAGACCA GCCTGACCAG CATGGTGGAA CCCCATCTC	660
TACTAAAAAC ACAAAAAATT AGCCGGGCGT GGTGGCACAT GCCTGTAATC CCAGCTACTC	720
AGGAGGCTGA GGCGGAGAAT TGCTTGAACC CGGAAGG	757

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 673 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CAGGACACAG AGTAAGATAC CCACTGACTT CTTGTGGTCT ACTTCCTGGG TGTGTTTCA	60
ATGGGCTTTG TTATAACAGG ACTAGTCTTC TGTAATATACA ACTTGGTAAA TAGGATGAAA	120
CATAACTTTG CGACAATTCA GTAGAAATAG GCATACAAAC CTGGGCCTGA TGACACTCAC	180
CTCCCCTTGG CTATAAACAT TACCCTACCT GTTAAGTCAG TAATCCTTTG GGAGAGCGCT	240
TACTGAGTAT CTATGATATG CAAAGACCAA AGACCGAGGG GGATCCCTGG TGTAGAGCAA	300

GCACACACCT GGTATTAGC TACCTGCCAC CCTGCTGGGC ATGCAACATA CATTGTCTCA 360
 AATTCTAACC ACCCTGCAAG GCAAGCTTCC TTGTTCTTTT AAAGAAGAAA AGTAGACCAG 420
 CAAGATTGAT TTGCTCAAGA TTACACAGCC TGGAACTTTG TCATGGGCAT GTCTGACTCT 480
 GATAGCAATA CCCTCAAAGA AACTGTCAGA GAAGACTCAA TAAGAAGAAA GTTGAGATAC 540
 AGAAACCAAC AGGAGAAGGT AATTCAGAAA TTCAAACAGA GTGGGTGTGA TGGGAAGAAT 600
 TCATTAATAA GAAGGTACCT CTGTAGAAAA ATCTTACCAG ACAGTCTGGA AGTGAAGGAA 660
 ACAGCCAATA GTC 673

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 358 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GTCACTGCAC ATTAAGATGG AGCCCGAAGA GCCACACTCC GAGGGGGCAT CGCAGGAGGA 60
 TGGGGCTCAA GGTGCCTGGG GCTGGGCACC CCTAAGTCAC GGCTCTAAGG AGAAAGCTCT 120
 CTTCTTGCCC GCGGAGCCC TCCCCTCCCC CCGGATCCCC GTGCTTTCCC GAGAGGGGAG 180
 GACCAGAGAC CGGCAGATGG CTGCAGCGCT CCTCACTGCC TGGTCCCAGA TGCCAGTGAC 240
 TTTCGAGGAT GTGGCCTTGT ACCTCTCCCG GGAGGAGTGG GGACGGCTGG ACCACACGCA 300
 GCAGAACTTC TACAGGGAAT GTCCTGCAGA AGAAAAATGG GCTGTCACTG GGCTTTCC 358

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CACAGATGTA GCTTCCTCAC TGG 23

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 610 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

CTGGAGTACA ATGTCAGTGT TTACACTGTC AAGGATGACA AGGAAAGTGT CCCTATCTCT	60
GATACCATCA TCCCAGCTGT TCCTCCTCCC ACTGACCTGC GATTCACCAA CATTGGTCCA	120
GACACCATGC GTGTCACCTG GGCTCCACCC CCATCCATTG ATTTAACCAA CTCCTGGTG	180
CGTTACTCAC CTGTGAAAAA TGAGGAAGAT GTTGCAGAGT TGTCAATTTC TCCTTCAGAC	240
AATGCAGTGG TCTTAACAAA TCTCCTGCCT GGTACAGAAT ATGTAGTGAG TGTCTCCAGT	300
GTCTACGAAC AACATGAGAG CACACCTCTT AGAGGAAGAC AGAAAACAGG TCTTGATTCC	360
CCAACTGGCA TTGACTTTTC TGATATTACT GCCAACTCTT TTACTGTGCA CTGGATTGCT	420
CCTCGAGCCA CCATCACTGG CTACAGGATC CGCCATCATC CCGAGCACTT CAGTGGGAGA	480
CCTCGAGAAG ATCGGGTGCC CCACTCTCGG AATTCCATCA CCCTCACCAA CCTCACTCCA	540
GGCACAGAGT ATGTGGTCAG CATCGTTGCT CTTAATGGCA GAGAGGAAAG TCCCTTATTG	600
ATTGGCCAAC	610

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1649 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CGGCAGCCAG CCTATTCTTT GGCCGGGTCG GTGCGAGTGG TCGGCTGGGC AGAGTGCACG	60
CTGCTTGGCG CCGCAGGTGA TCCCGCCGTC CACTCCCGGG AGCAGTGATG TTGGGCAACT	120
CTGCGCCGGG GCCTGCGACC CGCGAGGCGG GCTCGGCGCT GCTAGCATTG CAGCAGACGG	180
CGCTCCAAGA GGACCAGGAG AATATCAACC CGGAAAAGGC AGCGCCCGTC CAACAACCGC	240
GGACCCGGGC CGCGCTGGCG GTACTGAAGT CCGGGAACCC GCGGGGTCTA GCGCAGCAGC	300
AGAGGCCGAA GACGAGACGG GTTGCACCCC TTAAGGATCT TCCTGTAAAT GATGAGCATG	360
TCACCGTTCC TCCTTGAAAA GCAAACAGTA AACAGCCTGC GTTCACCATT CATGTGGATG	420

AAGCAGAAAA	AGAAGCTCAG	AAGAAGCCAG	CTGAATCTCA	AAAAATAGAG	CGTGAAGATG	480
CCCTGGCTTT	TAATTCAGCC	ATTAGTTTAC	CTGGACCCAG	AAAACCATTG	GTCCCTCTTG	540
ATTATCCAAT	GGATGGTAGT	TTTGAGTCAC	CACATACTAT	GGACATGTCA	ATTGTATTAG	600
AAGATGAAAA	GCCAGTGAGT	GTTAATGAAG	TACCAGACTA	CCATGAGGAT	ATTCACACAT	660
ACCTTAGGGA	AATGGAGGTT	AAATGTAAAC	CTAAAGTGGG	TTACATGAAG	AAACAGCCAG	720
ACATCACTAA	CAGTATGAGA	GCTATCCTCG	TGGACTGGTT	AGTTGAAGTA	GGAGAAGAAT	780
ATAAACTACA	GAATGAGACC	CTGCATTTGG	CTGTGAACTA	CATTGATAGG	TTCCTGTCTT	840
CCATGTCAGT	GCTGAGAGGA	AAACTTCAGC	TTGTGGGCAC	TGCTGCTATG	CTGTTAGCCT	900
CAAAGTTTGA	AGAAATATAC	CCCCCAGAAG	TAGCAGAGTT	TGTGTACATT	ACAGATGATA	960
CCTACACCAA	GAAACAAGTT	CTGAGAATGG	AGCATCTAGT	TTTGAAAGTC	CTTACTTTTG	1020
ACTTAGCTGC	TCCAACAGTA	AATCAGTTTC	TTACCCAATA	CTTTCTGCAT	CAGCAGCCTG	1080
CAAAC TGCAA	AGTTGAAAGT	TTAGCAATGT	TTTTTGGGAGA	ATTAAGTTTG	ATAGATGCTG	1140
ACCCATACCT	CAAGTATTTG	CCATCAGTTA	TTGCTGGAGC	TGCC'TTTCAT	TTAGCAC'TCT	1200
ACACAGTCAC	GGGACAAAGC	TGGCCTGAAT	CATTAATACG	AAAGACTGGA	TATACCCTGG	1260
AAAGTCTTAA	GCCTTGTCTC	ATGGACCTTC	ACCAGACCTA	CCTCAAAGCA	CCACAGCATG	1320
CACAACAGTC	AATAAGAGAA	AAGTACAAAA	ATTCAAAGTA	TCATGGTGTT	TCTCTCCTCA	1380
ACCCACCAGA	GACACTAAAT	CTGTAACAAT	GAAAGACTGC	CTTTGTTTTT	TAAGATGTAA	1440
ATCACTCAAA	GTATATGGTG	TACAGTTTTT	AAC'TTAGGTT	TTTAATTTTA	CAATCATTTT	1500
TGAATACAGA	AGTTGTGGCC	AAGTACAAAT	TATGGTATCT	ATTACTTTTT	AAATGGTTTT	1560
AATTTGTATA	TCTTTTGTAT	ATGTATCTGT	CTTAGATATT	TGGCTAATTT	TAAGTGGTTT	1620
TGTTAAAGTA	TTAATGATGC	CAGCTGCCG				1649

(2) INFORMATION FOR SEQ ID NO:9:

(xi) SEQUENCE DESCRIPTION: SEO ID NO:9:

TTCTGGGGCT CTTACTATAA AAGGGGACCA ACTCTCCCTT TGTCATATCT TGTTTCTGAT 120
GACAAAAAAT AACACATTGT TAAAATTGTA AAATTAAAC ATGAAATATA AATTA 175

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 166 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTTTCGCTCC ACATTCATCC TTTCTTACTG GGCACGTGATG TTGAGAGCAT CAGGCAGGGT 60
ATAATGTTAT GTTGCAGTAA CAAACACCCT CAATATCTCA GTGGCTTAAA ATGACAACGA 120
TCTTTTTTTTT GTTTGTTTGT TTATGCTCTA TATCACCCAG GGATCA 166

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 107 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGCTCTGCCC CACATCTGAA CAAGCTAATA AGAAAGCCCG ATGTTCTTTC CTTTGGTGCC 60
ATTGGGAAAT TCAAACCATG CACAACTCTG CCTGTATGAA GGGCGCA 107

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 183 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAACCTTAGC CCCTCTCCTC TTCTTCACGA TGCCATTCTG CCATTTCTGT TTTGTGGTAG 60
ACAGGTTGGC CCAGGCACTC TAAGGCCCCAG GCTGGCACAG GTTGGCCCCAG GCACTTCAAG 120
CCTAAGTCCA TTTACAGTTT CTATTCCATC TCTTCCTAAA GAAGAGGAGA GGGGCTAAGG 180

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 92 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AAACAAACGT CTTTGGGTAA AATTCTATTT CTTTAAATGT TTTAAAATAT TTGTAGTCAC 60
 TAATTGTAAG TCATATTCCT CTTTGTCCAG CT 92

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 182 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GATGTAATTA AAGCTGTAGA TGAGGGCTAT CGACTGCCAC CCCCCATGGA CTGCCCAGCT 60
 GCCTTGATATC AGCTGATGCT GGACTGCTGG CAGAAAGACA GGAACAACAG ACCCAAGTTT 120
 GAGCAGATTG TTAGTATTCT GGACAAGCTT ATCCGGAATC CCGGCAGCCT GAAGGATCAT 180
 CA 182

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 174 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GCCAAATGGG TAGCATTGTT GCTCGGCCTT CTAGTCTGCC AGTAGGAAAG TCCAACCATT 60
 AGGTCGGGGA AGAAGGGTCT GGATTTGGTT GACAATGGTT GGATGGGGGA TAGAAGCAGA 120
 GAGAGAGAGG GAGGGCAGCT CAAGGGTATC TTGCCCCACT CTGTTTATGC TGAT 174

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 132 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CACCTAACAA TATATCAATT TTTTAAAAAT GGAATTTCTT ATGCCCTCTT TATTTATGGA	60
CATGTATGTC CATAATGGGA GACGTTTTCT TTGGACTGAT GCTTGAATCA GTGGGTGCTT	120
GGCATTGCTG AT	132

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

CAGACACACA CATGCACACC ATTCTAGAAT GCTTCCTTAA AAGAAGGAGG GTTGCCCTAG	60
TCTCAAAATC TTAAGGCCA TATGTGCATT GATTTCTGCA CAGGTAGGCA ATTTGTGATT	120
TTATTTTTC TATG	135

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTCATGGCA GGACTCGGTT TGGG	24
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(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GGCCCCAAATG CCAGGCTGCA CTGATCTCAT GTCTGTGTCA CTGGAACCAA CAGGCCTGCC 60
TCAACCACTG TCCACCTGCA CATCTGAGAG GCTGGCAGGT CACCAGGGCT AGCCGTGCAC 120
GTCAGTTCCT GGGAAGAAAG TAGAATGTGA ATCATCTTCT CTCAAACGCC TATCAAAAAGC 180
CCAGCTGAGA TCAATAATTT GGTGGGAGAA CAGACCTGTA CCAATTGGCT CGGTGTTTGG 240
TGGGGTATTG TAAATTTGGA TCCTAAATCA AAGGGTATCC CTAGAAGGAC CCACATGGAA 300
TGGCCTCCTC CTAAACATCC CTCCATGTTG GTACTTCCTG ACTCTTTTCC AGCAATCTCA 360
AAGCACAAGA AGCAGTGGTG GGAACCCAGG CCTGGCATCT TGTGGAGCC CATGGTTGGG 420
GGGTAGGAGC AACTTTACAG GCCATCAATT ATGCCCTAT ACGCACCTCC C 471

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 209 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GCCCTTTATA AATACGATTA GTATGGAGAA TTGATACATT AACAGTTAGC TTTATAAATT 60
GACAGATTTT TAAATTAACC TATGGTCCAC AAATCAAGTT CTATCACTAT TTCCTGCCAC 120
CAAAATCAGT GATGAAGCCT CTCCCACACT AAATGAAGAG TGGCGAGGGA CAGAATTCCA 180
CTTGTCTTCC TTTTGCTGCA CTAACATA 209

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 407 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CAAGCAGCAT AGCCTCTCTG AACTCAATT TCCTCACATT TATAAATGAG CTTTTATATT 60
ATTTACAAAC CTACCTCATA GAGCAGGTTG CAGGCTACAT GAGAAGGTGC AAGTTCAATG 120
CCAAGCAGGG TCCTAGTATT TAATAAAAGC TCAATAAATA TTCATTTTCT TCTTTCCTTC 180

TCTTACTTGA AGTATAACAT TTGATAATGA ATTTTCTCAT TGCAACAATA ACACCCCTTC	240
CACTGAGGGA TTTGTATCCC TGCTTAAGAA GCTATTAGTA TTCTACAGCA GGA CTCACCC	300
CACACAATCT TGGCAGGAAT ACATCCCTCT ACCTCTCTGG TCAATAACCT GCCTGGCCTG	360
TGACCCCAGG CTTCTGGAG AAGCACCAAG TCCTCCCAGT TTCCCCC	407

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 267 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CATTGGTGCA GCAGGTTTAG ATGGCTATGT GCTAGAGTAT TGCTTTGAAG GAAGTAAGTA	60
CAACCAGTAG ATAAAATGAA TACTGTCATC AATAGGTGAG ATATGTCCCT CCCCTTTCTG	120
TTGTCTCTCT TTCTTGAGAA CGCATCACCT TCCTACGAAA ATAAGATCAA GCCAAACGTC	180
ATCCTTCTGA GATGTATATA AACTAAGCCC TTTTITAGTA CTTGGTGCTT ATAAATTGAT	240
ATCTCAAAAG TATCTTGGCT AGGCTGC	267

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 333 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATAGTCCAG GAGCAGAGTT AGCCAGAATT GCCTCCTGCT GCCCCAGCTT AGAGAGCTCC	60
CATCTCAATC ATTGAGCCTG AAGGCTTCAA GCCCAAATG CAACAAGACC CCCAGCCTAC	120
ATTTCTCAGC TCCCCTGGAG CCAGTGATCC TGTAACGCTG CTGGAGGTCA GTCTGAGCTA	180
CCAAGACTGT CCCTAGACAA AGGTGGGAGT CCCCCACACT GCCAAGACCA AATCCCTCAC	240
TCAACCTGCT GAGGTGTTGG ATGGGGAAAC AAGAGGCAAA ACTGAGGCAC CTGATGCATT	300
CAGCCCTGCT TGTGCAGAAG TGCATTGACT GCC	333

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CCTGTGGCGT AAGGCATCCC A

21

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GCAAGCACTC CTTTGTA AAA TGTCC

25

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGCGTTCACC ATTCATGTGG ATGAAGCAG

29

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

CTCCTACTTC AACTAACCAG TCCACGAG

28

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GATGCTTTGA AGTTATCTCT CTTGG

25

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATCAGTGTGG CAGATATAAT GGACC

25

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GCCCCAAATG CCAGGCTGCA CTGAT

25

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GCCAGAAGAC AAGAGTGTGA GCCTT

25

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

GCTTCAGGGT GGTCCAATTA GAGTT

25

(2) INFORMATION FOR SEQ ID NO:33:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TCCAACAACG ACACATTCAG GAGTT

25

(2) INFORMATION FOR SEQ ID NO:34:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GGACACAGAG TAAGATACCC ACTGA

25

(2) INFORMATION FOR SEQ ID NO:35:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

CCTCGGTCTT TGGTCTTTGC ATATC

25

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACAAGGAAAG TGTCCCTATC TCTGA

25

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

CTCGAGGTCT CCCACTGAAG TGCTC

25

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

CACTGCACAT TAAGATGGAG CCCGA

25

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

CCTGTAGAAG TTCTGCTGCG TGTGG

25

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGAGCTGCCT GACGGCCAGG TCATC

25

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

GAAGCATTTG CGGTGGACGA TGGAG

25

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

TAGAAGACCA AATGCCCCGA GT

22

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

TGTATTTCTG TGGGATCGGT GG

22

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 369 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CCATAAGAGA AATGATTGGT AGGTTTGCAT GAAATTTTAA AATTCCTGT GGCCTAAGGC	60
ATCCCATAAC GAAGCCAAAA GGTGAGTGAT AGACTGGGAG AAATAACTGC CAGACGTTGC	120
CAGACAAAGA TTTCATATTT CTAATATGCT AGAGTACCTT TAATTTGATA AGAAAAAGAT	180
AAGCAATCCT GTAATAAAAT GGACATTTTA CAAAGGAGTG CTTGCAAATG GCCAGTGAAT	240
TTATGCAAAT ATGTTTCAGGG AAATAGGAAT GAAAACGAGA TTCCACTTTT TCATCATCCA	300
TTTGATTGGC AAGAAATTTT TAAAAGAGTA ATACCTAGTG AATCACTCAT GTAGGAAAAT	360
GGGTTGGTG	369

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 301 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: modified_base
- (B) LOCATION: 212
- (D) OTHER INFORMATION: /note= "N = A, C, G, or T"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

GCCCTTGAAG AGTGTAACCA AGAAGCATCT CTCAATCAAT GAACCTGAGA CAGCCTGTTC	60
ACTTCTGACC ATCATTCTTG TCCTTTAGAT CTCAGTTTCA AATTCATTTC TTCTAGACAT	120
TCATCTCTTC CCATGTTTAA TCTGGAACCA TCTACCCTTC CACCAGACCA ATTATCCTGG	180
CAAATTAATG TAATAGACCA GTATTAATTA TMTGGTTGTA TGTCTTAACA ACATTCTAGG	240
TGCTGTGCCA AAAACAAATG AATAGCAACA CAAGGTCTTC TTGGTTACAC TCTTCAAGGG	300
C	301

(2) INFORMATION FOR SEQ ID NO:47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3061 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 15..1172

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

CGGCTCTCCT CAAC ATG AGA GCT GCA CCC CTC CTC CTG GCC AGG GCA GCA	50
Met Arg Ala Ala Pro Leu Leu Leu Ala Arg Ala Ala	
1 5 10	
AGC CTT AGC CTT GGC TTC TTG TTT CTG CTT TTT TTC TGG CTA GAC CGA	98
Ser Leu Ser Leu Gly Phe Leu Phe Leu Leu Phe Phe Trp Leu Asp Arg	
15 20 25	
AGT GTA CTA GCC AAG GAG TTG AAG TTT GTG ACT TTG GTG TTT CGG CAT	146
Ser Val Leu Ala Lys Glu Leu Lys Phe Val Thr Leu Val Phe Arg His	
30 35 40	
GGA GAC CGA AGT CCC ATT GAC ACC TTT CCC ACT GAC CCC ATA AAG GAA	194
Gly Asp Arg Ser Pro Ile Asp Thr Phe Pro Thr Asp Pro Ile Lys Glu	
45 50 55 60	
TCC TCA TGG CCA CAA GGA TTT GGC CAA CTC ACC CAG CTG GGC ATG GAG	242
Ser Ser Trp Pro Gln Gly Phe Gly Gln Leu Thr Gln Leu Gly Met Glu	
65 70 75	
CAG CAT TAT GAA CTT GGA GAG TAT ATA AGA AAG AGA TAT AGA AAA TTC	290
Gln His Tyr Glu Leu Gly Glu Tyr Ile Arg Lys Arg Tyr Arg Lys Phe	
80 85 90	
TTG AAT GAG TCC TAT AAA CAT GAA CAG GTT TAT ATT CGA AGC ACA GAC	338
Leu Asn Glu Ser Tyr Lys His Glu Gln Val Tyr Ile Arg Ser Thr Asp	
95 100 105	
GTT GAC CGG ACT TTG ATG AGT GCT ATG ACA AAC CTG GCA GCC CTG TTT	386
Val Asp Arg Thr Leu Met Ser Ala Met Thr Asn Leu Ala Ala Leu Phe	
110 115 120	
CCC CCA GAA GGT GTC AGC ATC TGG AAT CCT ATC CTA CTC TGG CAG CCC	434
Pro Pro Glu Gly Val Ser Ile Trp Asn Pro Ile Leu Leu Trp Gln Pro	
125 130 135 140	
ATC CCG GTG CAC ACA GTT CCT CTT TCT GAA GAT CAG TTG CTA TAC CTG	482
Ile Pro Val His Thr Val Pro Leu Ser Glu Asp Gln Leu Leu Tyr Leu	

145					150					155						
CCT	TTC	AGG	AAC	TGC	CCT	CGT	TTT	CAA	GAA	CTT	GAG	AGT	GAG	ACT	TTG	530
Pro	Phe	Arg	Asn	Cys	Pro	Arg	Phe	Gln	Glu	Leu	Glu	Ser	Glu	Thr	Leu	
160					165					170						
AAA	TCA	GAG	GAA	TTC	CAG	AAG	AGG	CTG	CAC	CCT	TAT	AAG	GAT	TTT	ATA	578
Lys	Ser	Glu	Glu	Phe	Gln	Lys	Arg	Leu	His	Pro	Tyr	Lys	Asp	Phe	Ile	
175					180					185						
GCT	ACC	TTG	GGA	AAA	CTT	TCA	GGA	TTA	CAT	GGC	CAG	GAC	CTT	TTT	GGA	626
Ala	Thr	Leu	Gly	Lys	Leu	Ser	Gly	Leu	His	Gly	Gln	Asp	Leu	Phe	Gly	
190					195					200						
ATT	TGG	AGT	AAA	GTC	TAC	GAC	CCT	TTA	TAT	TGT	GAG	AGT	GTT	CAC	AAT	674
Ile	Trp	Ser	Lys	Val	Tyr	Asp	Pro	Leu	Tyr	Cys	Glu	Ser	Val	His	Asn	
205					210					215					220	
TTC	ACT	TTA	CCC	TCC	TGG	GCC	ACT	GAG	GAC	ACC	ATG	ACT	AAG	TTG	AGA	722
Phe	Thr	Leu	Pro	Ser	Trp	Ala	Thr	Glu	Asp	Thr	Met	Thr	Lys	Leu	Arg	
225					230					235						
GAA	TTG	TCA	GAA	TTG	TCC	CTC	CTG	TCC	CTC	TAT	GGA	ATT	CAC	AAG	CAG	770
Glu	Leu	Ser	Glu	Leu	Ser	Leu	Leu	Ser	Leu	Tyr	Gly	Ile	His	Lys	Gln	
240					245					250						
AAA	GAG	AAA	TCT	AGG	CTC	CAA	GGG	GGT	GTC	CTG	GTC	AAT	GAA	ATC	CTC	818
Lys	Glu	Lys	Ser	Arg	Leu	Gln	Gly	Gly	Val	Leu	Val	Asn	Glu	Ile	Leu	
255					260					265						
AAT	CAC	ATG	AAG	AGA	GCA	ACT	CAG	ATA	CCA	AGC	TAC	AAA	AAA	CTT	ATC	866
Asn	His	Met	Lys	Arg	Ala	Thr	Gln	Ile	Pro	Ser	Tyr	Lys	Lys	Leu	Ile	
270					275					280						
ATG	TAT	TCT	GCG	CAT	GAC	ACT	ACT	GTG	AGT	GGC	CTA	CAG	ATG	GCG	CTA	914
Met	Tyr	Ser	Ala	His	Asp	Thr	Thr	Val	Ser	Gly	Leu	Gln	Met	Ala	Leu	
285					290					295					300	
GAT	GTT	TAC	AAC	GGA	CTC	CTT	CCT	CCC	TAT	GCT	TCT	TGC	CAC	TTG	ACG	962
Asp	Val	Tyr	Asn	Gly	Leu	Leu	Pro	Pro	Tyr	Ala	Ser	Cys	His	Leu	Thr	
305					310					315						
GAA	TTG	TAC	TTT	GAG	AAG	GGG	GAG	TAC	TTT	GTG	GAG	ATG	TAC	TAT	CGG	1010
Glu	Leu	Tyr	Phe	Glu	Lys	Gly	Glu	Tyr	Phe	Val	Glu	Met	Tyr	Tyr	Arg	
320					325					330						
AAT	GAG	ACG	CAG	CAC	GAG	CCG	TAT	CCC	CTC	ATG	CTA	CCT	GGC	TGC	AGC	1058
Asn	Glu	Thr	Gln	His	Glu	Pro	Tyr	Pro	Leu	Met	Leu	Pro	Gly	Cys	Ser	
335					340					345						
CCT	AGC	TGT	CCT	CTG	GAG	AGG	TTT	GCT	GAG	CTG	GTT	GGC	CCT	GTG	ATC	1106
Pro	Ser	Cys	Pro	Leu	Glu	Arg	Phe	Ala	Glu	Leu	Val	Gly	Pro	Val	Ile	
350					355					360						

TCTAAGTGCC TCCAAGTTCA AAACCTTATTG GAATGTTGAG AGTGTGGTTA CGAAATACGT 2642
TAGGAGGACA AAAGGAATGT GTAAGTCTTT AATGCCGATA TCTTCAGAAA ACCTAAGCAA 2702
ACTTACAGGT CCTGCTGAAA CTGCCCCACTC TGCAAGAAGA AATCATGATA TAGCTTTCCA 2762
TGTGGCAGAT CTACATGTCT AGAGAACACT GTGCTCTATT ACCATTATGG ATAAAGATGA 2822
GATGGTTTCT AGAGATGGTT TCTACTGGCT GCCAGAATCT AGAGCAAAGC CATCCCCCCT 2882
CCTGGTTGGT CACAGAATGA CTGACAAAGA CATCGATTGA TATGCTTCTT TGTGTTATTT 2942
CCCTCCCAAG TAAATGTTTG TCCTTGGGTC CATTTTCTAT GCTTGTAACGT GTCTTCTAGC 3002
AGTGAGCCAA ATGTAAAATA GTGAATAAAG TCATTATTAG GAAGTTCAAA AAAAAAAAAA 3061

(2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 386 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Met	Arg	Ala	Ala	Pro	Leu	Leu	Leu	Ala	Arg	Ala	Ala	Ser	Leu	Ser	Leu	1	5	10	15
Gly	Phe	Leu	Phe	Leu	Leu	Phe	Phe	Trp	Leu	Asp	Arg	Ser	Val	Leu	Ala	20	25	30	
Lys	Glu	Leu	Lys	Phe	Val	Thr	Leu	Val	Phe	Arg	His	Gly	Asp	Arg	Ser	35	40	45	
Pro	Ile	Asp	Thr	Phe	Pro	Thr	Asp	Pro	Ile	Lys	Glu	Ser	Ser	Trp	Pro	50	55	60	
Gln	Gly	Phe	Gly	Gln	Leu	Thr	Gln	Leu	Gly	Met	Glu	Gln	His	Tyr	Glu	65	70	75	80
Leu	Gly	Glu	Tyr	Ile	Arg	Lys	Arg	Tyr	Arg	Lys	Phe	Leu	Asn	Glu	Ser	85	90	95	
Tyr	Lys	His	Glu	Gln	Val	Tyr	Ile	Arg	Ser	Thr	Asp	Val	Asp	Arg	Thr	100	105	110	
Leu	Met	Ser	Ala	Met	Thr	Asn	Leu	Ala	Ala	Leu	Phe	Pro	Pro	Glu	Gly	115	120	125	
Val	Ser	Ile	Trp	Asn	Pro	Ile	Leu	Leu	Trp	Gln	Pro	Ile	Pro	Val	His	130	135	140	

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

TCGCTCCACA TTCATCCTTT CT

22

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

TGATCCCTGG GTGATATAGA GCATA

25

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GCCCCACATC TGAACAAGCT AATAA

25

(2) INFORMATION FOR SEQ ID NO:52:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

TGCGCCCTTC ATACAGGCAG AGTTG

25

(2) INFORMATION FOR SEQ ID NO:53:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

CACGATGCCA TTCTGCCATT TCTGT

25

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

GGAAGAGATG GAATAGAAAC TGTAAC

25

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 23 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

CTTAACTCGG GCATTGGTC TTC

23

(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS:

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys Ala Thr Glu Phe Ile

1

5

10

15

Asp Tyr Ser Ile Glu

20

(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

149

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

CACTGGAACC AACAGGCCTG CCTCAAC

27

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

CCGAGCCAAT TGGTACAGGT CTGTTCTCCC

30

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

CCTCAAGACT GGTCCACGGA GTGTATGA

28

(2) INFORMATION FOR SEQ ID NO:60:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

GGGTAATGGC CAAAGTATGT TCTCAAAGCA

30

(2) INFORMATION FOR SEQ ID NO:61:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

AAACAAACGT CTTTGGGTAA A

21

(2) INFORMATION FOR SEQ ID NO:62:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CTGGACAAAG AGGAATATGA

20

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

GCCCTTTATA AATACGATTA GTATGGAG

28

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

TGTAGTTAGT GCAGCAAAAG GAAGA

25

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

GATGTAATTA AAGCTGTAGA TGAGGG

26

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

GAATACTAAC AATCTGCTCA AACTTGGG

28

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

GCCAAATGGG TAGCATTGTT GCTCGG

26

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

CAGAGTGGGG CAAGATACCC TTGAG

25

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

AATGGAATTT CTTATGCCCT C

21

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

CAATGCCAAG CACCCACTGA TTC

23

(2) INFORMATION FOR SEQ ID NO:71:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

ACACAGACAC ACACATGCAC ACCA

24

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

CCTACCTGTG CAGAAATCAA

20

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

AGCAGCATAG CCTCTCTGAA ACTC

24

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 27 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

CCTTCTCATG TAGCCTGCAA CCTGCTC

27

(2) INFORMATION FOR SEQ ID NO:75:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CATTGGTGCA GCAGGTTTAG ATGG

24

(2) INFORMATION FOR SEQ ID NO:76:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 25 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

GAGATATCAA TTTATAAGCA CCAAG

25

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

ATCTCAATCA TTGAGCCTGA AGG

23

(2) INFORMATION FOR SEQ ID NO:78:

154

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

CAGCAGGTTG AGTGAGGGAT TTGG

24

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

CGCCTCAGGC TGGGGCAGCA TT

22

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGTGGAAG AGTCTCATTC GAGAT

25

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

CGAGCTGCCT GACGGCCAGG TCATC

25

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

GAAGCATTTG CGGTGGACGA TGGAG

25

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2087 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 99..503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

GACCTTAAAT ATATCGAGGT GGCTAATTGA TGTATAATAA TTTACAAAAT TATTCTTCTA	60
TTGCTACAGA GCTACAATTC AATTTACAGT AGGCCACC ATG AGG GCC TTC TTA	113
Met Arg Ala Phe Leu	
1 5	
AGG AAC CAG AAA TAT GAG GAT ATG CAC AAT ATT ATT CAC ATT TTA CAG	161
Arg Asn Gln Lys Tyr Glu Asp Met His Asn Ile Ile His Ile Leu Gln	
10 15 20	
ATC AGA AAA TTG AGG CAC AGA TTA AGT AAC TTC CCA AGG CTA CCA GGC	209
Ile Arg Lys Leu Arg His Arg Leu Ser Asn Phe Pro Arg Leu Pro Gly	
25 30 35	
ATT CTA GCT CCA GAA ACT GTG CTC TTA CCA TTC TGC TAC AAG GTA TTT	257
Ile Leu Ala Pro Glu Thr Val Leu Leu Pro Phe Cys Tyr Lys Val Phe	
40 45 50	
CGA AAA AAA GAA AAA GTA AAA AGA AGT CAA AAG GCA ACA GAG TTC ATT	305
Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys Ala Thr Glu Phe Ile	
55 60 65	
GAT TAT TCC ATA GAA CAG TCA CAC CAT GCA ATT CTC ACA CCC TTG CAG	353
Asp Tyr Ser Ile Glu Gln Ser His His Ala Ile Leu Thr Pro Leu Gln	
70 75 80 85	
ACA CAC TTG ACC ATG AAA GGT TCC TCA ATG AAA TGT TCC TCA TTA TCT	401
Thr His Leu Thr Met Lys Gly Ser Ser Met Lys Cys Ser Ser Leu Ser	
90 95 100	

TCA GAA GCC ATA TTA TTC ACA TTG ACT TTG CAG TTA ACT CAG ACC CTA	449
Ser Glu Ala Ile Leu Phe Thr Leu Thr Leu Gln Leu Thr Gln Thr Leu	
105 110 115	
GGT CTG GAA TGC TGT CTT CTC TAC TTA TCC AAA ACT ATA CAT CCA CAG	497
Gly Leu Glu Cys Cys Leu Leu Tyr Leu Ser Lys Thr Ile His Pro Gln	
120 125 130	
ATC ATA TAAACTCTCA GCCCTGCTGC AAAGCCTTTC CAGAAAAATA AAAATGGTTG	553
Ile Ile	
135	
AAAAGGCAAT TCTGCTACCA ATGACTGTTT AAGCCCAGCC AAGTAACTGA ACCATTCCAA	613
CTTCAATTTA CTTATGAAAA GAATTTGATG ATGTAGGAGG TTATTTCAAT TCTAAAATAC	673
AAACCCATGT TGATCTTTCT CAATCTTGAA CTCATAGATT ATTATCTATT ATCTCAATTT	733
AGTTTGTTAT TTATCCTAGT GGGCCATTAA AACTACCAC ATGTGTTTCT GTCTCTCCAT	793
TAGTCAATAA CTAAACTAAC GAGCAATTAG TAAGCCATGT GCCAGATGCT CCGCTAGGCA	853
CCAGAGGGAT AAAACAATA CTTATAGTAT ACCACTAATT TTCGCTTAGT AACTAGTGAA	913
ATGTTCAAGT CATGCCTGAG TCAAGAGTTG AGGAGACATT ACAATGTGTA ATGGAAACCA	973
AGGAAAAGTGA AACTTTGGAT AAGTGGGGAC TAGTGTATTT ATATATTTAA TTGATTTCTG	1033
ACTCTATCAT TGGCCTCCAA ACACAGATTG TGTTTTTCTT TGGTTTTGTT TTCTTCACTA	1093
TGGGATCTTC TGTGCCCAGC ACAGTGCCTG ACACATAGAA AACAATCAAT ATTTGCTGAA	1153
TAAATGATTA AAAAATCAGA GAACTTTCCC ATTCTGTTTG GATCTATAGA ACATCCAGAG	1213
TAAGTGATGA GGGCCTCTGC ATTTATATGC GCTTAAATTA AGATTATGTG AGAAAAGTTT	1273
AAAGACACTT AGTAGAGTGA TTTTGAAATA TAGTAAACAC TTGGAAATGG TGGTGCTTTA	1333
AAAAGATATT AATAGATAAT ATGAAAATCT CCATCTCAAA AATAATGCAT AACTATTTA	1393
AAGGAAAATC ACATCTCCAG GCTTTCAATG TTTGTTTCATT ACTTTTTTCAT ATATTTTTAC	1453
CATCTGCTGA AGGCAGTCAT ATCAAAGGGT AAAGAAAGAT GGGAGGAAAA CTCAGTAAGA	1513
ATTATATTAG TCTGTTTGCA AAGTAGAAAA AGATTCTCAT CACTCAACCT TATGAGCAGG	1573
AAGAGGGAAG GCTGTTTGAG AACCATTTAC TTAGCAGAAC CACATATTTT AGACACTTCC	1633
CTGCATTAAC TGCACAAACA ATATGTTTGC AAAGTTGTTG ATCAACCTCC AACAACGACA	1693
CATTGAGGAG TTAAATATTT TTCATCAAAC ATTGGATTTT TCCTTAACGC TAGAGATTGC	1753
TACAAATCTT CTGAAGGGTC TCAATGGCTT CAGGCTAAGA AGAGATTTCT CCCTGTTATA	1813

AGCAGCAAGA CAAATTAGCC ATTTCACTCT CAACTTCAC TAATGATCAC ATTCTTTCCA 1873
 AAAGGAACTC TAGAAGACCA AATGCCCGGA GTTAAGAACA TCAAACTAA CCATCTGAAG 1933
 AAAGTTCCCA AGTGTAAGAC TCTGCCTGCA CGACAACACA TAAAAAAGA GAGAAGAATC 1993
 AAATAGACAC AATAAAAAAT GATAAAGGGG ATATCACCAC CGATCCCACA GAAATACAAA 2053
 CTACCATCAG AGAATACTAC AAACACCTCT ACGC 2087

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

Met	Arg	Ala	Phe	Leu	Arg	Asn	Gln	Lys	Tyr	Glu	Asp	Met	His	Asn	Ile	1	5	10	15
Ile	His	Ile	Leu	Gln	Ile	Arg	Lys	Leu	Arg	His	Arg	Leu	Ser	Asn	Phe	20	25	30	
Pro	Arg	Leu	Pro	Gly	Ile	Leu	Ala	Pro	Glu	Thr	Val	Leu	Leu	Pro	Phe	35	40	45	
Cys	Tyr	Lys	Val	Phe	Arg	Lys	Lys	Glu	Lys	Val	Lys	Arg	Ser	Gln	Lys	50	55	60	
Ala	Thr	Glu	Phe	Ile	Asp	Tyr	Ser	Ile	Glu	Gln	Ser	His	His	Ala	Ile	65	70	75	80
Leu	Thr	Pro	Leu	Gln	Thr	His	Leu	Thr	Met	Lys	Gly	Ser	Ser	Met	Lys	85	90	95	
Cys	Ser	Ser	Leu	Ser	Ser	Glu	Ala	Ile	Leu	Phe	Thr	Leu	Thr	Leu	Gln	100	105	110	
Leu	Thr	Gln	Thr	Leu	Gly	Leu	Glu	Cys	Cys	Leu	Leu	Tyr	Leu	Ser	Lys	115	120	125	
Thr	Ile	His	Pro	Gln	Ile	Ile										130	135		

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2505 base pairs

(B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ix) FEATURE:

(A) NAME/KEY: CDS
 (B) LOCATION: 99..503

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GACCTTAAAT ATATCGAGGT GGCTAATTGA TGTATAATAA TTTACAAAAT TATTCTTCTA	60
TTGCTACAGA GCTACAATTC AATTTACAGT AGGCCACC ATG AGG GCC TTC TTA	113
Met Arg Ala Phe Leu	
1 5	
AGG AAC CAG AAA TAT GAG GAT ATG CAC AAT ATT ATT CAC ATT TTA CAG	161
Arg Asn Gln Lys Tyr Glu Asp Met His Asn Ile Ile His Ile Leu Gln	
10 15 20	
ATC AGA AAA TTG AGG CAC AGA TTA AGT AAC TTC CCA AGG CTA CCA GGC	209
Ile Arg Lys Leu Arg His Arg Leu Ser Asn Phe Pro Arg Leu Pro Gly	
25 30 35	
ATT CTA GCT CCA GAA ACT GTG CTC TTA CCA TTC TGC TAC AAG GTA TTT	257
Ile Leu Ala Pro Glu Thr Val Leu Leu Pro Phe Cys Tyr Lys Val Phe	
40 45 50	
CGA AAA AAA GAA AAA GTA AAA AGA AGT CAA AAG GCA ACA GAG TTC ATT	305
Arg Lys Lys Glu Lys Val Lys Arg Ser Gln Lys Ala Thr Glu Phe Ile	
55 60 65	
GAT TAT TCC ATA GAA CAG TCA CAC CAT GCA ATT CTC ACA CCC TTG CAG	353
Asp Tyr Ser Ile Glu Gln Ser His His Ala Ile Leu Thr Pro Leu Gln	
70 75 80 85	
ACA CAC TTG ACC ATG AAA GGT TCC TCA ATG AAA TGT TCC TCA TTA TCT	401
Thr His Leu Thr Met Lys Gly Ser Ser Met Lys Cys Ser Ser Leu Ser	
90 95 100	
TCA GAA GCC ATA TTA TTC ACA TTG ACT TTG CAG TTA ACT CAG ACC CTA	449
Ser Glu Ala Ile Leu Phe Thr Leu Thr Leu Gln Leu Thr Gln Thr Leu	
105 110 115	
GGT CTG GAA TGC TGT CTT CTC TAC TTA TCC AAA ACT ATA CAT CCA CAG	497
Gly Leu Glu Cys Cys Leu Leu Tyr Leu Ser Lys Thr Ile His Pro Gln	
120 125 130	
ATC ATA TAAACTCTCA GCCCTGCTGC AAAGCCTTTC CAGAAAAATA AAAATGGTTG	553
Ile Ile	
135	
AAAAGGCAAT TCTGCTACCA ATGACTGTTT AAGCCCAGCC AAGTAACTGA ACCATTCCAA	613

CTTCAATTTA	CTTATGAAAA	GAATTTGATG	ATGTAGGAGG	TTATTTCAAT	TCTAAAATAC	673
AAACCCATGT	TGATCTTTCT	CAATCTTGAA	CTCATAGATT	ATTATCTATT	ATCTCAATTT	733
AGTTTGTTAT	TTATCCTAGT	GGGCCATTAA	AAACTACCAC	ATGTGTTTCT	GTCTCTCCAT	793
TAGTCAATAA	CTAAACTAAC	GAGCAATTAG	TAAGCCATGT	GCCAGATGCT	CCGCTAGGCA	853
CCAGAGGGAT	AAAAACAATA	CTTATAGTAT	ACCACTAATT	TTCGCTTAGT	AACTAGTGAA	913
ATGTTCAAGT	CATGCCTGAG	TCAAGAGTTG	AGGAGACATT	ACAATGTGTA	ATGGAAACCA	973
AGGAAAGTGA	AACTTTGGAT	AAGTGGGGAC	TAGTGTATTT	ATATATTTAA	TTGATTTCTG	1033
ACTCTATCAT	TGGCCTCCAA	ACACAGATTG	TGTTTTTCTT	TGGTTTTGTT	TTCTTCACTA	1093
TGGGATCTTC	TGTGCCCAGC	ACAGTGCCTG	ACACATAGAA	AACAATCAAT	ATTTGCTGAA	1153
TAAATGATTA	AAAAATCAGA	GAACTTTCCC	ATTCTGTTTG	GATCTATAGA	ACATCCAGAG	1213
TAAGTGATGA	GGGCCTCTGC	ATTTATATGC	GCTTAAATTA	AGATTATGTG	AGAAAAGTTT	1273
AAAGACACTT	AGTAGAGTGA	TTTTGAAATA	TAGTAAACAC	TTGGAAATGG	TGGTGCTTTA	1333
AAAAGATATT	AATAGATAAT	ATGAAAATCT	CCATCTCAAA	AATAATGCAT	AACTATTTA	1393
AAGGAAAATC	ACATCTCCAG	GCTTTCAATG	TTTGTTTCATT	ACTTTTTCAT	ATATTTTTAC	1453
CATCTGCTGA	AGGCAGTCAT	ATCAAAGGGT	AAAGAAAGAT	GGGAGGAAAA	CTCAGTAAGA	1513
ATTATATTAG	TCTGTTTGCA	AAGTAGAAAA	AGATTCTCAT	CACTCAACCT	TATGAGCAGG	1573
AAGAGGGAAG	GCTGTTTGAG	AACCATTTAC	TTAGCAGAAC	CACATATTTT	AGACACTTCC	1633
CTGCATTAAC	TGCACAAACA	ATATGTTTGC	AAACTTGTTG	ATCAACCTCC	AACAACGACA	1693
CATTCAGGAG	TTAAATATTT	TTCATCAAAC	ATTGGATTTT	TCCTTAACGC	TAGAGATTGC	1753
TACAAATCTT	CTGAAGGGTC	TCAATGGCTT	CAGGCTAAGA	AGAGATTTCT	CCCTGTTATA	1813
AGCAGCAAGA	CAAATTAGCC	ATTTCACTCT	CAAACCTCAC	TAATGATCAC	ATTCCTTTCCA	1873
AAAGGAACTC	TAGAAGACCA	AATGCCCCGA	GTTAAGAACA	TCAAACTAA	CCATCTGAAG	1933
AAACTTCCCA	AGTGTAAGAC	TCTGCCATTA	AAACATTACC	GAGAGGGGAC	TCAAACAGTC	1993
TTTCTTCCTT	TGTCGTGTTT	CTTGCTCCCA	GACCAAGGCA	CTGACGACAG	TACTGATACA	2053
TAATTTAAAA	GCACACTCCC	TTCCACTTTG	GTAATACCAG	AACTCTAATT	GGACCACCCT	2113
GAAGCTTAGG	ACTACCAGCC	ATACAAATAG	TAAACTCTGT	CCACGATTCA	CTCATCTGTG	2173
TATTTTCTAT	AGATGTTTAC	TAGGCGTTTG	TTATATAAAA	ATACCCCGGC	CAGGCACGGT	2233

GGCTCACGCC TGTAATCCCA GCACTTTGGG AGGTGGGTGG ATCACCTGAG GTCGGGAGTT 2293
 CGAGACCAGC CTGACCAGCA TGGTGGGAACC CCCATCTCTA CTAAAAACAC AAAAAATTAG 2353
 CCGGGCGTGG TGGCACATGC CTGTAATCCC AGCTACTCAG GAGGCTGAGG CGGAGAATTG 2413
 CTTGAACCCG GAAGGTGGAG GTTGTTCGGG TGAGCTGAGA TTGCACTATT GCACTCCAGC 2473
 CTGGGCAACA GGAGTAAAC TCCCCCCCAC CC 2505

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

Met	Arg	Ala	Phe	Leu	Arg	Asn	Gln	Lys	Tyr	Glu	Asp	Met	His	Asn	Ile	1	5	10	15
Ile	His	Ile	Leu	Gln	Ile	Arg	Lys	Leu	Arg	His	Arg	Leu	Ser	Asn	Phe	20	25	30	
Pro	Arg	Leu	Pro	Gly	Ile	Leu	Ala	Pro	Glu	Thr	Val	Leu	Leu	Pro	Phe	35	40	45	
Cys	Tyr	Lys	Val	Phe	Arg	Lys	Lys	Glu	Lys	Val	Lys	Arg	Ser	Gln	Lys	50	55	60	
Ala	Thr	Glu	Phe	Ile	Asp	Tyr	Ser	Ile	Glu	Gln	Ser	His	His	Ala	Ile	65	70	75	80
Leu	Thr	Pro	Leu	Gln	Thr	His	Leu	Thr	Met	Lys	Gly	Ser	Ser	Met	Lys	85	90	95	
Cys	Ser	Ser	Leu	Ser	Ser	Glu	Ala	Ile	Leu	Phe	Thr	Leu	Thr	Leu	Gln	100	105	110	
Leu	Thr	Gln	Thr	Leu	Gly	Leu	Glu	Cys	Cys	Leu	Leu	Tyr	Leu	Ser	Lys	115	120	125	
Thr	Ile	His	Pro	Gln	Ile	Ile										130	135		

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CCCACCTCCC AAAGTGCTGG GA

22

TOTAL: 945453